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Entrez
PubMed

1: Mol Gen Genet 1998 Feb;257(4):387-91

[Related Articles](#), [Books](#), [LinkOut](#)**COP1b, an isoform of COP1 generated by alternative splicing, has a negative effect on COP1 function in regulating light-dependent seedling development in Arabidopsis.**PubMed
Services**Zhou DX, Kim YJ, Li YF, Carol P, Mache R.**Laboratoire de Genetique Moleculaire des Plantes, Universite Joseph Fourier,
Grenoble, France.Related
Resources

COP1 is a negative regulator of Arabidopsis light-dependent development. Mutation of the COP1 locus causes constitutive photomorphogenesis in the dark. Here, we report the identification of an isoform of the COP1 protein, named COP1b, which is generated by alternative splicing. COP1b has a 60-amino acid deletion in the WD-40 repeat domain relative to the full-length COP1. This splicing step is light-independent and takes place mostly in mature seeds and in germinating seedlings. Transgenic Arabidopsis plants that overexpress COP1b show a de-etiolated phenotype in the dark, with a short hypocotyl, open and developed cotyledons. The transgenic seedlings are adult-lethal. These phenotypes closely resemble that of severe cop-1 mutants, indicating that COP1b has a dominant negative effect on COP1 function.

PMID: 9529519 [PubMed - indexed for MEDLINE]

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BLAST PubMed Nucleotide Protein Genome Structure Taxonomy Help

Query: gi|2326943 *Xenopus laevis* mRNA for Fizzy-related protein, and translated products

Lineage: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; *Xenopus*

All hits Common Tree Taxonomy Report 3D structures CDD-Search GI list

22 BLAST hits to 6 unique species in *Viridiplantae* Sort by taxonomy proximity

0 Archaea 70 Bacteria 44 Metazoa 45 Fungi 22 Plants 0 Viruses 4 Other Eukaryotae

Keep only ☐ Cut-Off 100

493 aa

	SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
16					
-----	1249	3	AAF37386	7158292	WD-repeat cell cycle regulatory prote
-----	1248	3	AAD22612	4558462	cell cycle switch protein [Medicago
-----	1240	3	AAM20437	20466239	putative fizzy-related protein [Arab:
-----	1240	3	CAA19806	3292816	putative fizzy-related protein [Arab:
-----	1237	3	AAL36231	17380838	putative Srw1 protein [Arabidopsis th
1					
-----	1215	3	CAB44330	5002527	Srw1-like protein [Arabidopsis thali
-----	1192	3	BAB11112	10177650	cell cycle switch protein [Arabidops:
-----	1191	3	AAM20433	20466231	cell cycle switch protein [Arabidops:
4					
-----	893	3	BAB63690	15289995	putative cell cycle switch protein [C
2					
-----	882	3	CAB38784	4490293	WD-repeat protein-like protein [Arab:
-----	867	3	CAA11819	3668118	hypothetical protein [Brassica napus]
12					
-----	807	3	NP_198109	15240985	cdc20-like protein [Arabidopsis thal:
1					
-----	791	3	AAB63030	2253631	WD-repeat protein [Daucus carota]
-----	786	3	NP_198060	15240441	putative cdc20 protein [Arabidopsis t
-----	786	3	AAD48933	5732032	contains similarity to Pfam family PI
-----	784	3	NP_198042	15240403	WD-repeat protein - like [Arabidopsi
-----	782	3	AAB61049	2191163	contains similarity to beta transduc:
3					
-----	735	3	AAF14048	6491862	putative cdc20 protein [Arabidopsis t
-----	729	3	CAB38785	4490294	WD-repeat protein-like protein [Arab:
1					
-----	680	3	NP_568505	18421178	WD-repeat protein - like [Arabidopsi
123					



Blast 2 Sequences results

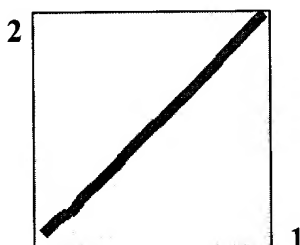
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.1.2 [Oct-19-2000]

Matrix BLOSUM62 ☐ gap open: 11 gap extension: 1
x_dropoff: 50 expect: 300. wordsize: 3 Filter ☐ Align

Sequence 1 gi 7290520 fzf gene product [Drosophila melanogaster] Length 478 (1 .. 478)

Sequence 2 gi 10177650 Length 472 (1 .. 472)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 457 bits (1164), Expect = e-127

Identities = 237/445 (53%), Positives = 286/445 (64%), Gaps = 18/445 (4%)

```
Query: 23  NNFESSTPTSLDRFIPCRAYNNWQTNFASINKSNDNSPQTSKKQDCGETARDSLAYSC 82
          ++ S + T DRFIPCR+ + D P T K+ + AYS
Sbjct: 35  SSLSSPSKSTCSDRFIPCRSSRLHAF----DLQDKEPTTPVKEGG-----NEAYSR 82

Query: 83  LLKNELLGSAIDDV---KTAGEERNENAYTPAAKRSLFKYQSPTKQDYNGECPYSLSPVS 139
          LLK+EL GS G+ + +P FK + P L +
Sbjct: 83  LLKSELFGSDFASPLLSPAGGQGSASSPMSPCTNMLRFKTDTSNSSPSPFSPSILGNDN 142

Query: 140 AKSQKLLRSPRKATRKISRIPFKVLDAPELQDDFYLNLDWSSQNVLAVGLGSCVYLWSA 199
          S P K RK+ + P KVLDAP LQDDFYLN+VDWSSQNVLAVGLG+CVYLW+A
Sbjct: 143 GHSSDS-SPPPKPPRKVPKTPHKVLDAPELQDDFYLNVDWSSQNVLAVGLGTCVYLWTA 201

Query: 200 CTSQVTRLCDLSPDANTVTSVSWNERGNTVAVGTHHGVTVDVAANKQINKLNHGSARV 259
          S+VT+LCDL P+ ++V SV W G+ +++GT HG V VWD K++ + GH R
Sbjct: 202 SNSKVTKLCDLGPN-DSVCSVQWTREGSYISIGTSHGQVQVWDGTQCKRVRTMGGHQTRT 260

Query: 260 GALAWNSDILSSGSRDRWIIQRDTRTPQLQSERRLAGHRQEVCGLKWSPDNQYLASGGND 319
          G LAWNS ILSSGSRDR I+Q D R Q +L GH+ EVCGLKWS D++ LASGGND
Sbjct: 261 GVLAWNSRILSSGSRDRNILQHDIRV-QSDFVSKLVGHKSEVCGLKWSHDDRELASGGND 319

Query: 320 NRLYVWNQHSVNPVQSYTEHMAAVKAIASPHHHGLLASGGGTADRCIRFWNTLTGQPMQ 379
          N+L VWN HS P+ TEH AAVKAI WSPH LLASGGGTADRCIRFWNT G +
Sbjct: 320 NQLLVWNNHSQQPILKLTEHTAAVKAITWSPHQSSLLASGGGTADRCIRFWNTTNGNQLN 379

Query: 380 CVDTG SQVCNLAWSKHSSSELVSTHGYSQNQILVWKYPSLTQVAKLTGHSYRVLYLALSPD 439
          +DTGSQVCNLAWSK+ +E+VSTHGYSQNQI++WKYPS+++VA LTGHS RVLYLA SPD
Sbjct: 380 SIDTG SQVCNLAWSKNVNEIVSTHGYSQNQIMLVKYPMSKVVATLTGHSMRVLYLATSPD 439

Query: 440 GEAIVTGAGDETLRFWNVFSKARSQ 464
          G+ IVTGAGDETLRFWNVF + Q
```

Sbjct: 440 GQTIVTGAGDETLRFWNVFPVSKMQ 464

CPU time: 0.37 user secs. 0.04 sys. secs 0.41 total secs.

Gapped

Lambda	K	H
0.314	0.129	0.393

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 2391

Number of Sequences: 0

Number of extensions: 159

Number of successful extensions: 16

Number of sequences better than 300.0: 1

Number of HSP's better than 300.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 472

length of database: 181,542,687

effective HSP length: 55

effective length of query: 417

effective length of database: 160,388,367

effective search space: 66881949039

effective search space used: 66881949039

T: 9

A: 40

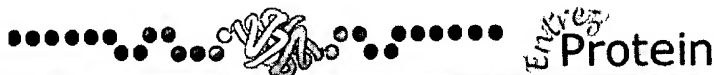
X1: 16 (7.2 bits)

X2: 128 (49.9 bits)

X3: 128 (49.9 bits)

S1: 42 (22.0 bits)

S2: 60 (27.8 bits)



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	Books
Search <input type="text" value="Nucleotide"/> for <input type="text"/>							<input type="button" value="Go"/>	<input type="button" value="Clear"/>
		Limits	Preview/Index	History	Clipboard		Details	
Display <input type="text" value="default"/>		<input type="button" value="Save"/>	<input type="button" value="Text"/>	<input type="button" value="Add to Clipboard"/>				

1: BAB11112. cell cycle switch...[gi:10177650] [BLink, Nucleotide, Related Sequences, PubMed, Taxonomy, LinkOut](#)

LOCUS BAB11112 472 aa linear PLN 27-DEC-2000
 DEFINITION cell cycle switch protein [Arabidopsis thaliana].
 ACCESSION BAB11112
 VERSION BAB11112.1 GI:10177650
 DBSOURCE locus AB005230 accession [AB005230.2](#)
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (sites)
 AUTHORS Sato,S., Kotani,H., Nakamura,Y., Kaneko,T., Asamizu,E., Fukami,M.,
 Miyajima,N. and Tabata,S.
 TITLE Structural analysis of Arabidopsis thaliana chromosome 5. I.
 Sequence features of the 1.6 Mb regions covered by twenty
 physically assigned P1 clones
 JOURNAL DNA Res. 4 (3), 215-230 (1997)
 MEDLINE 97471969
 PUBMED 9330910
 REFERENCE 2 (residues 1 to 472)
 AUTHORS Nakamura,Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUL-1997) Yasukazu Nakamura, Kazusa DNA Research
 Institute, Department of Plant Gene Research; 1532-3, Yana,
 Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
 Tel:81-438-52-3935, Fax:81-438-52-3934)
 COMMENT Address for correspondence: kaos@kazusa.or.jp
 For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MAC12
 Genes with similarity to proteins in the databases are described in
 'product' or 'note' qualifiers. Genes that have no significant
 protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Grail
 (Informatics Group, Oak Ridge National Laboratory,
<http://compbio.ornl.gov/Grail-1.3/>),
 GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>),
 NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
 Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and
 SplicePredictor (Volker Brendel, Stanford University,
<http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi>).
 Genes encoding tRNAs are predicted by tRNAscan-SE
 (Sean Eddy, Washington University School of Medicine, St. Louis,
<http://genome.wustl.edu/eddy/tRNAscan-SE/>).
 This sequence may not be the entire insert of this clone. It may be
 shorter because we remove overlaps between neighboring submissions.
 The 5' clone is MXE10 and the 3' clone is MUA22.
 FEATURES Location/Qualifiers
 source 1..472
 /organism="Arabidopsis thaliana"
 /strain="Columbia"

Protein

CDS

/db_xref="taxon:3702"
/chromosome="5"
/clone="MAC12"
/clone_lib="Mitsui P1"
1..472
/product="cell cycle switch protein"
1..472
/coded_by="complement(join(AB005230.2:19277..19435,
AB005230.2:19524..19820,AB005230.2:19943..20185,
AB005230.2:20272..20376,AB005230.2:20468..20590,
AB005230.2:20688..21179))"
/note="gene_id:MAC12.21"

ORIGIN

1 maspqstktg lnlpagmnqt slrletfsss frgisslssp skstcsdrfi pcrsssrilha
61 fdlqdkeptt pvkeggneay srllkselfg sdfasp1lsp aggggsassp mspctnmlrf
121 ktdrsnssps spfspsilgn dnghssdssp ppkpprkvpk tphkvldaps lqddfylnvv
181 dwssqnv1av glgtcvylwt asnskvtklc dlgpndsvcs vqwtregsyi sigtshgqvq
241 vwdgtqckrv rtmgghqtrt gvlawnsril ssgsrdrnil qhdirvqsdf vsklvghkse
301 vcglkwshdd relasggndn qllvwnnhsq qpilklteht aavkaitwsp hqssllasgg
361 gtadrcirfw nttngnqlns idtgsqvcnl awsknvneiv sthgysqnqi mlwkypsmask
421 vatltghsmr vlylatspd g qtivtgagde tlrfnvfps vkmqvcilfs sl

//

Revised: October 24, 2001.

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